REMARKS

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made."

New claims 22-29 correspond substantially to the "polynucleotide inventions" previously under consideration and include recitations which were characterized as raising "new issues" by the Advisory Action of April 2, 2001. New claims 30-34 define methods of using the polynucleotides defined by claims 24 and 28. By the Commissioner's Notice in the Official Gazette of March 26, 1996, entitled "Guidance on Treatment of Product and Process Claims in light of *In re Ochiai, In re Brouwer* and 35 U.S.C. § 103(b)", the Patent Office has set forth criteria for rejoining non-elected method claims upon allowance of product claims. In the present case, rejoinder of claims 30-34 would appear proper upon allowance of the polynucleotide claims since those method claims are dependent on product claims 24 and 28.

In light of the above amendments and remarks, Applicants submit that the present application is fully in condition for allowance, and request that the Examiner withdraw the outstanding rejections. Early notice to that effect is earnestly solicited.

If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact Applicants' Attorney at (650)855-0555.

Applicants believe that no fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Deposit Account No. **09-0108. This form is enclosed in duplicate.**

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS:

Claims 3, 5-7 and 9-12 have been canceled.

The following new claims 22-34 have been added:

22. An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence of SEQ ID NO:1,

b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1,

c) a biologically active fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1, and

d) an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1.

23. An isolated polynucleotide encoding a polypeptide of SEQ ID NO:1.

24. An isolated polynucleotide of claim 23 comprising the sequence of SEQ ID NO:2.

25. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 22.

26. A cell transformed with a recombinant polynucleotide of claim 25.

27. A method for producing a polypeptide encoded by a polynucleotide of claim 22, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell

is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide of claim 22, and

b) recovering the polypeptide so expressed.

28. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence of SEQ ID NO:2,

b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence of SEQ ID NO:2,

c) a polynucleotide complementary to the polynucleotide of a),

d) a polynucleotide complementary to the polynucleotide of b), and

e) an RNA equivalent of a)-d).

29. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 28.

30. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 28, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

31. A method of claim 30, wherein the probe comprises at least 60 contiguous nucleotides.

32. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 28, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

33. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 24, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

34. A method for assessing toxicity of a test compound, said method comprising:

a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 28 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 28 or fragment thereof;

c) quantifying the amount of hybridization complex; and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.